

2314-227
JLI:ch

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

10862 U.S. PTO
09/749637
12/28/00

In re patent application of:)
Baldomero M. OLIVERA)
Serial No.: (to be assigned))
Filed: 28 December 2000)
For: O-SUPERFAMILY CONOTOXIN)
PEPTIDES)

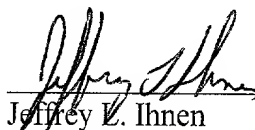
STATEMENT PURSUANT TO 37 CFR 1.821(f)

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

In the matter of the above-identified application, which is filed concurrently herewith, Applicants submit a computer diskette containing the Sequence Listing of the instant application. It is hereby certified that the paper and computer copies of these sequences are identical.

Respectfully submitted,



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Jones, Robert M.
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<130> 2314-227

<151> 2000-10-27

<151> 2000-07-20

<151> 2000-06-26

<151> 1999-12-30

<160> 409

<170> PatentIn version 3.0

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Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
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ttt ccg aag gcg ggt cac gaa atg gag aac ctc gaa gtc tct aat cgg 144
Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
35 40 45

gtc aag ccg tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa 192
Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
50 55 60

aac tgc tgc cgt ggc tgg aat tgc gtt ott ttc tgc gtc tgaaactacc 241
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 1 5 10 15

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Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
 35 40 45

Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
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 <213> Conus omaria

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<400> 8

Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys
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 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser
 10 15 20 25

aga aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag 147
 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu
 30 35 40

aac ctc gaa gac tct aaa cac agg cac cag gag aga ccg gac acc ggc 195
 Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly
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gac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa 243

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Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
20 25 30

ttt tgc aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc gtt cca cac gag ggc cct tgt aat tgg ctt aca caa 192
Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
50 55 60

aac tgc tgc agt ggt tat aat tgc atc att ttt ttc tgc cta 234
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20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
50 55 60

Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu

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 <212> PRT
 <213> Conus omaria

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Cys Val Xaa His Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
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 <213> Conus dalli

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 tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
 20 25 30
 ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45
 agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60
 cag aga cag gtc aag ccg tgt cgt aaa gaa cat caa ctt tgt gat ctg 240
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
 65 70 75 80
 att ttt caa aac tgc tgc cgt ggc tgg tat tgc ttg ctt cgt cct tgc 288
 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys
 85 90 95
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 Ile

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<400> 16

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 20 25 30

Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60

Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
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Ile

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<223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 4 and 29
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<221> SITE

<222> (1)..(31)

<223> Xaa at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

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 1 5 10 15

Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Leu Leu Arg Xaa Cys Ile
 20 25 30

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 <212> DNA
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 tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
 20 25 30
 ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45
 agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60
 cag aga cgg gtc aag ccg tgc agt gaa gaa ggt caa ctt tgt gat cca 240
 Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
 65 70 75 80
 ctt tct caa aac tgc tgc cgt ggc tgg cat tgc gtt ctt gtc tct tgc 288
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 gtc tgaaactacc gtgatgtott ctctcccatc 321
 Val

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 <212> PRT
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 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 35 40 45
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 50 55 60
 Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
 65 70 75 80

003327" / E964/60

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 20 25 30

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 Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
 15 20 25

ttg ggg aat ctt ttt tgg aat gca cat cac gaa atg aag aac ccc gaa 145
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 30 35 40

gcc tct aaa ttg aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt 193
 Ala Ser Lys Leu Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys
 45 50 55 60

aat ttg tta gac caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc 241
 Asn Leu Leu Asp Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val
 65 70 75

tgc aca taaaactgcc gtgatgtctt ctct ccct ctgtgtacc tggcttgatc 297
 Cys Thr

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tttgattggc gcggtgctgtt cactgggttat gaaccccccc cccccccccc cccccccct 357

tccggctctc tggaggcctc gggggttcaa catccaaata aagtgacag 406

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<400> 22

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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

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50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

<210> 23
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<212> PRT
<213> Conus textile

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<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 23

Xaa Cys Lys Gln Asp Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
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Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
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<212> PRT
<213> Conus textile

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Glu or gamma-carboxy-Glu; Xaa at residue 9 is Nle; Xaa at residue
20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T

00822T 429460

<400> 24

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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

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35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp

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Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
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 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 27

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Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

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 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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 20 25

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 <213> Conus distans

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tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96

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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
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 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60
 caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234
 Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75
 taaaactgcc gtgatgtctt ctctccct c 265

<210> 30
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<400> 30

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 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
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<220>
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 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr

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 tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30
 ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60
 caa aac tgc tgc gag ggc tat tgc ata gta ctt gtc tgc aca 234
 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75
 taaaactgcc gtgatgtctt ctctccct c 265

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 <213> Conus ammiralis

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 1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
 20 25 30
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
 50 55 60
 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
 65 70 75

<210> 34
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<212> PRT
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<220>
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<400> 34

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
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Cys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr
 20 25

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<220>
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 tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct aag ttg aat 144
 Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
 35 40 45
 gag agg tgc ctt ggt ggt ggt gaa gtt tgt gat atc ttt ttt cca caa 192
 Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
 50 55 60
 tgc tgt ggc tat tgc att ctt ctt ttc tgc aca taaaactacc gtgatgtcctt 245
 Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
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 ctctctccct c 256

<210> 36
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<400> 36

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

094963 12300

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
35 40 45

Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
50 55 60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
65 70 75

<210> 37
<211> 25
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-
Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 37

Cys Leu Gly Gly Gly Xaa Val Cys Asp Ile Phe Phe Xaa Gln Cys Cys
1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Thr
20 25

<210> 38
<211> 441
<212> DNA
<213> Conus gloriamaris

<220>
<221> CDS
<222> (70)..(300)

<400> 38
gcttgcaacgg tgaatttggc ttcacagttt tccactgtcg tctttggcat catctgaaac 60

atcgccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 111
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 159
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
15 20 25 30

aat att ttt tcg aat gca cat cac gaa atg aag aat ccc gaa gcc tct 207
Asn Ile Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac aag agg tgc cgt cta ggg gct gaa agt tgt gat gta att 255
Lys Leu Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile
50 55 60

00949637-122800

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<210> 41
<211> 446
<212> DNA
<213> Conus gloriamaris
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<222> (74) .. (304)

ggatccttgc acggtgaatt tggcttcaca gttttccact gtcgtctttc gcatcatcca 60

ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac ccc aga aat gga 157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

ttg gag aaa ctt ttt tcg aat aca cat cac gaa atg aag aac ccc gaa 205
Leu Glu Lys Leu Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu
30 35 40

gcc tct aaa ttg aac aag agg tgc aaa caa gct gat gaa tct tgt aat 253
Ala Ser Lys Leu Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn
45 50 55 60

gta ttt tca ctt gac tgc tgc acc ggc tta tgc ttg gga ttc tgc gta 301
Val Phe Ser Leu Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val
65 70 75

tog t^gatgtcttc tactccoctc t^gt^gctacct ggcttgatct ttgattggcg 354
Ser

tgtgcctttc attggttatg aacccccctg atccgattct ttggcggcct cggggggttca 414

acatccaaat aaagcgacag cacaataaaa aa 446

<213> Conus gloriamaris

<400> 42

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Lys Leu
20 25 30

Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn Val Phe Ser Leu
50 55 60

Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
65 70 75

<210> 43


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<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.
```

Cys Lys Gln Ala Asp Xaa Ser Cys Asn Val Phe Ser Leu Asp Cys Cys
1 5 10 15
Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
20 25

```
<220>
<221> CDS
<222> (1)..(225)
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[illegible]

<400> 45

Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
20 25 30

Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
35 40 45

Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
50 55 60

Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
65 70 75

<210> 46
<211> 25
<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 2 and 7 may be Pro or hydroxy-Pro; Xaa at residue
4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-ca
rboxy-Glu ; Xaa at residue 10 may be Trp or bromo-Trp

<400> 46

Cys Val Xaa Xaa Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
1 5 10 15

Asp Xaa Leu Cys Val Phe Phe Cys Leu
20 25

<210> 47
<211> 250
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(231)

<400> 47
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctc ttc ttg acc gtc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val
1 5 10 15

tgg aca ttc gcc acg gct gat gac tcc gga aat gga ttg gag aaa ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc aaa caa gct gat gaa cct tgt gat gta ttt tca ctt 192
Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
50 55 60

gaa tgc tgc acc ggc ata tgt ctt gga ttc tgc acg tgg tgatgtcttc 241
Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

002227 4696450

250

<400> 48

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
50 55 60

Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

<210>	49
<211>	26
<212>	PRT
<213>	Conus magus

```
<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at r
      esidue 7 may be Pro or hydroxy-Pro; Xaa at residue 26may be Trp o
      r bromo-Trp
```

<400> 49

Cys Lys Gln Ala Asp Xaa Xaa Cys Asp Val Phe Ser Leu Xaa Cys Cys
1 5 10 15

Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa
20 25

```
<210> 50
<211> 434
<212> DNA
<213> Conus textile
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```
<220>
<221> CDS
<222> (71)..(295)
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<400> 50
gccttgcaag gtgaatttgg cttcatagtt ttccactgtc gtctttggca tcatccaaaa 60
catcaccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 109
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<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.
```

<400> 52

Cys Leu Asp Ala Gly Xaa Val Cys Asp Ile Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Ala
20 25

<210> 53
<211> 26
<212> PRT
<213> Conus textile

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at residue 7 may be Pro or hydroxy-Pro

<400> 53

Cys Ile Xaa Gln Phe Asp Xaa Cys Xaa Met Ile Arg His Thr Cys Cys
1 5 10 15

Val Gly Val Cys Phe Leu Met Ala Cys Ile
20 25

<210> 54
<211> 26
<212> PRT
<213> Conus textile

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 54

Cys Ala Xaa Phe Leu His Xaa Cys Thr Phe Phe Phe Xaa Asn Cys Cys
1 5 10 15

Asn Ser Xaa Cys Val Gln Phe Ile Cys Leu
20 25

<210> 55
<211> 260
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (1)..(240)

<400> 55

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Leu Ala Xaa His Xaa Thr Cys Asn Ile Phe Thr Gln Asn Cys Cys
1 5 10 15

Xaa Gly Val Cys Ile Phe Ile Cys Val Gln Ala Xaa Xaa
 20 25

<210> 58
 <211> 261
 <212> DNA
 <213> Conus omaria

<220>
 <221> CDS
 <222> (1)..(231)

<400> 58
 atg aaa ctg act gtc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttt gcc acg gct gaa gac ccc aga cat gga ttg gag aat ctt 96
 Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
 20 25 30
 ttt tcg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
 35 40 45
 gac aag agg tgc att cca cat ttt gac cct tgt gac ccg ata cgc cac 192
 Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
 50 55 60
 acc tgc tgc ttt ggc ctg tgc cta cta ata gcc tgc atc taaaactgcc 241
 Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 65 70 75
 gtgatgtctt ctctcccatc 261

<210> 59
 <211> 77
 <212> PRT
 <213> Conus omaria

<400> 59
 Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
 35 40 45
 Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
 50 55 60
 Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 65 70 75

<210> 60

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<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.
```

Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
1 5 10 15
Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
20 25

```
<220>
<221> CDS
<222> (1)..(228)
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```
<210> 62
<211> 76
<212> PRT
<213> Conus omaria
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Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
20 25 30

262

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
50 55 60

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

```
<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 4 and 6 may be Glu or gamma-carboxy-Glu; Xaa at re
      sidue 28 may be Pro or hydroxy-Pro
```

<400> 66

Cys Lys Ala Xaa Asn Xaa Leu Cys Asn Ile Phe Ile Gln Asn Cys Cys
1 5 10 15

Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Xaa Gln
20 25

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<210> 67
<211> 258
<212> DNA
<213> Conus aulicus
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```
<220>
<221> CDS
<222> (1) .. (228)
```

<400> 67

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

```

<210> 68
<211> 76
<212> PRT
<213> Conus aulicus

<400> 68

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1          5          10          15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
          20          25          30

Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu
          35          40          45

Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
          50          55          60

Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
65          70          75

```

<400> 69

Cys Leu Xaa Phe Gly Xaa Leu Cys Asn Phe Phe Phe Xaa Thr Cys Cys

1	5	10	15	
Gly Xaa Cys Val Leu Leu Val Cys Leu				
	20	25		
<210>	70			
<211>	263			
<212>	DNA			
<213>	Conus dalli			
<220>				
<221>	CDS			
<222>	(1)..(231)			
<400>	70			
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc				48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala				
1	5	10	15	
tgg aca ttt gtc atg gct gat gac tcc gga aat gga ttg gaa aat ctg				96
Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu				
	20	25	30	
ttt tgc aag gca cat cac gaa atg aag aac cct gaa gcc tct aaa ttg				144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu				
	35	40	45	
aac aag agg tgc gct caa agc agt gaa tta tgt gat gcg ctg gac tca				192
Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser				
50	55	60		
gac tgc tgc agt ggt gtt tgc atg gta ttt ttc tgc cta taaaactgcc				241
Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu				
65	70	75		
gtgatgtctt ctctatcccc tc				
				263
<210>	71			
<211>	77			
<212>	PRT			
<213>	Conus dalli			
<400>	71			
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala				
1	5	10	15	
Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu				
	20	25	30	
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu				
	35	40	45	
Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser				
50	55	60		
Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu				
65	70	75		

<210> 72
 <211> 26
 <212> PRT
 <213> Conus dalli

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

<400> 72

Cys Ala Gln Ser Ser Xaa Leu Cys Asp Ala Leu Asp Ser Asp Cys Cys
 1 5 10 15

Ser Gly Val Cys Met Val Phe Phe Cys Leu
 20 25

<210> 73
 <211> 259
 <212> DNA
 <213> Conus distans

<220>
 <221> CDS
 <222> (1)..(228)

<400> 73
 atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg agg aat ctt 96
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
 20 25 30
 tta tgc aat gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca 192
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
 50 55 60
 gac tgc tgc agc tat tgc gtt ggt gct gtc tgc cta taaaactacc 238
 Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
 65 70 75
 gtgatgtctt ctactcccat c 259

<210> 74
 <211> 76
 <212> PRT
 <213> Conus distans

<400> 74

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

003227" 2E964260

atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gct tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac gag agg tgc ctt ggg ttt ggt gaa gtt tgc aat ttc ttt ttt cca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta taaaactacc 238
Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

gtgatgtctt ctattccct c 259

<210> 80
<211> 76
<212> PRT
<213> Conus pennaceus

<400> 80

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

<210> 81
<211> 25
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I
-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 81

agg tgc ctt gac ggt ggt gaa att tgt ggt att ttg ttt cca agc tgc 163
 Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro Ser Cys
 5 10 15

tgc agt ggg tgg tgc att gtt ctc gtc tgc gca tgaaactacc gtgatgtctt 216
 Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 20 25 30

ctactcccct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 276

catgcgacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 336

acaacgtcgt gactgggaaa accctggcgt taccctaactt aatcgccttg cagcacatcc 396

ccctttcgcc agctggcgta atagcgaaga ggcccgacc gatcgccctt cccaacaagt 456

tgcgcagcct gaatggcgaa tgggacgcgc cctgtagcgg cgcattaagc gcggcggggtg 516

tggtggttac gcgcaccgtg accgctacac ttgccagcgc cctagccgcc cgctcctttc 576

gctttcttcc ctctctttct cgcacgttcg gccggctttc cccgtcaagc tctaaatcgg 636

gggcttcctt tttt 650

<210> 92

<211> 30

<212> PRT

<213> Conus omaria

<400> 92

Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe
 1 5 10 15

Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 20 25 30

<210> 93

<211> 26

<212> PRT

<213> Conus omaria

<220>

<221> SITE

<222> (1)..(26)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 mo-Trp

<400> 93

Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
 1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
 20 25

<210> 94

<211> 618

003221" 2E96460

<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (107)..(193)

<400> 94
ggtcgacatc atcatcatcg atccatctgt ccattccatcc atccattcat tcgctgccag 60
actgtaataa atattcgagt ctctctttct gtttgtatct gacaga ttg aac aag 115
Leu Asn Lys
1
agg tgc ctt gag ttt ggt gaa gtt tgt aat ttt ttt ttc cca acc tgc 163
Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe Pro Thr Cys
5 10 15
tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaaactacc gtgatgtctt 213
Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25
ctactcccct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 273
catgcgacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 333
acaacgtcgt gactgggaaa accctggcgt taccctaaactt aatcgccttg cagcacatcc 393
ccctttcggc agctggcgta atagcgaaga ggcccgcacc gatcgccctt cccaacagtt 453
gcgagcgtg aatggcgaaat gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt 513
ggtggttacg cgcagcgtga ccgtacact tgcagcgccc tagcgccgcg tcctttcgtc 573
ttcttccctt cctttctcgc cacgttcgcc ggctttcccc gtcaa 618

<210> 95
<211> 29
<212> PRT
<213> Conus marmoreus

<400> 95
Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
1 5 10 15
Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25

<210> 96
<211> 25
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 96

Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
 1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu
 20 25

<210> 97

<211> 444

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (150)..(236)

<400> 97

gaaagctggg acgcctgcag gtaccgggtcc ggaattcccg ggctcgacatc atcatcatca 60

togatccatc tgtccatcca tccattcatt cattcgctgc cagaactgtaa taaatattcg 120

agttttctcct tctgtttgta tctgacagg ttg aac aag agg tgc caa gag ttc 173
 Leu Asn Lys Arg Cys Gln Glu Phe
 1 5

ggg gaa gtt tgt aat ttt ttt ttc cca gac tgc tgc ggc tat tgc gtt 221
 Gly Glu Val Cys Asn Phe Phe Phe Pro Asp Cys Cys Gly Tyr Cys Val
 10 15 20

ctt tta ctc tgc ata taaaactacc gtgatgtctt ctcttcccat ctagtagtag 276
 Leu Leu Leu Cys Ile
 25

tagtagtagt aggcggccgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc 336

atagctcttc tatagtgtca cctaaattca attcactggc cgtcgtttta caaccgtcgt 396

gactgggaaa accctggcgt tcccaactta attcgcccttg cagcacat 444

<210> 98

<211> 29

<212> PRT

<213> Conus marmoreus

<400> 98

Leu Asn Lys Arg Cys Gln Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
 1 5 10 15

Pro Asp Cys Cys Gly Tyr Cys Val Leu Leu Leu Cys Ile
 20 25

<210> 99

<211> 25

<212> PRT

<213> Conus marmoreus

<220>

003327 4E96H260

<220>
 <221> misc_feature
 <222> (1)..(545)
 <223> n may be any nucleotide

<400> 101

Leu Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg
 1 5 10 15

His Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 20 25 30

<210> 102
 <211> 26
 <212> PRT
 <213> Conus omaria

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

<400> 102

Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
 1 5 10 15

Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
 20 25

<210> 103
 <211> 534
 <212> DNA
 <213> Conus omaria

<220>
 <221> CDS
 <222> (140)..(226)

<400> 103
 ggtacgcctg caggtaccgg tccggaattc ccgggtcgac atcatcatca tcgatccatc 60
 tgtccatcca tccattcttt catttgctgc cagactgtaa taaatattcg agtctctctt 120
 tctgttttga tctgacaga ttg aac aag agg tgc ctt gag ttt ggt gaa gtt 172
 Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val
 1 5 10
 tgt aat ttt ttt ttc cca acc tgc tgc ggc tat tgc gtt ctt ctt gtc 220
 Cys Asn Phe Phe Phe Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val
 15 20 25
 tgc cta taaaactacc gtgatgtctt ctcttccct ctagtagtag taggcggccg 276
 Cys Leu
 ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc 336
 acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt 396

002227.295460

tacccaactt aatcgcccttg cagcacatcc ccctttcgcc agctggcgta atagcgaaga 456
 ggcccgacc gatcgccctt cccaacagtt ggcagcctg aatggcgaat gggacgcgcc 516
 ctgtagcggc gcattaag 534

<210> 104
 <211> 29
 <212> PRT
 <213> Conus omaria

<400> 104

Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
 1 5 10 15

Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
 20 25

<210> 105
 <211> 25
 <212> PRT
 <213> Conus omaria

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
 esidue13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
 o-Tyr

<400> 105

Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
 1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu
 20 25

<210> 106
 <211> 200
 <212> DNA
 <213> Conus obscurus

<220>
 <221> CDS
 <222> (73)..(180)

<400> 106
 cgatccatct gtccatccat ccattcgctt gtctgctgcc aaactgtaat aaataaccga 60

gtctctctgt tt gta tct gac aga tcg aaa aag caa tgc cgt caa aat ggt 111
 Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly
 1 5 10

gaa gtg tgt gat gcg aat ttg gca cac tgc tgc agt ggc ccg tgt ttt 159
 Glu Val Cys Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe
 15 20 25

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35 40 45

aac aag agg tgc act caa agc ggt gaa ctt tgt gat gtg ata gac cca 192
 Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
 50 55 60

gac tgc tgc aat aat ttt tgc att ata ttt ttc tgc ata taaaactgcc 241
 Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
 65 70 75

gtgatgtctt ctactccct c 262

<210> 110
 <211> 77
 <212> PRT
 <213> Conus ammiralis

<400> 110

Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
 50 55 60

Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
 65 70 75

<210> 111
 <211> 26
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro

<400> 111

Cys Thr Gln Ser Gly Xaa Leu Cys Asp Val Ile Asp Xaa Asp Cys Cys
 1 5 10 15

Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
 20 25

<210> 112
 <211> 286
 <212> DNA
 <213> Conus textile

008222T "LE964260

<400> 112

<400> 113

<220>

<221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 114

Cys Ala Xaa Phe Leu His Leu Cys Thr Phe Phe Phe Xaa Asn Cys Cys
 1 5 10 15

Asn Gly Xaa Cys Val Gln Phe Ile Cys Leu
 20 25

<210> 115
 <211> 484
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (74)..(304)

<400> 115
 ggatcctagc acagtgaatt tggcttcaca gttttccact gtcgtctttg gcatcatcca 60
 aaacatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
 1 5 10
 ttc ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 157
 Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
 15 20 25
 ttg gag aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc aaa 205
 Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys
 30 35 40
 gac tct aaa ttg aac aag agg tgc ctt gac gct ggt gaa atg tgt gat 253
 Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp
 45 50 55 60
 ctt ttt aat tca aaa tgc tgc agt ggg tgg tgc att att ctc ttc tgc 301
 Leu Phe Asn Ser Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys
 65 70 75
 gca taaaactacc gtgatgtctt ctactcccct ctgtgctacc tggcttgatc 354
 Ala
 tttgattggc gcgtgccctt cactgggttat gaacccccct gatccgactc tctggcggcc 414
 tcggggggttc aacatccaaa taaagccgac acgatactga cgtagaaaaa aaaaaaaaaa 474
 aaaaaaaaaa 484

<210> 116
 <211> 77
 <212> PRT
 <213> Conus marmoreus
 <400> 116

003231 " 486460

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp Leu Phe Asn Ser
50 55 60

Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys Ala
65 70 75

<210> 117

<211> 26

<212> PRT

<213> Conus marmoreus

<220>

<221> SITE

<222> (1)..(26)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
19 may be Trp or bromo-Trp

<400> 117

Cys Leu Asp Ala Gly Xaa Met Cys Asp Leu Phe Asn Ser Lys Cys Cys
1 5 10 15

Ser Gly Xaa Cys Ile Ile Leu Phe Cys Ala
20 25

<210> 118

<211> 427

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (19)..(249)

<400> 118

gccgaaaaca tcaccaaag atg aaa ctg acg agc atg atg atc gtt gct gtg 51
Met Lys Leu Thr Ser Met Met Ile Val Ala Val
1 5 10

ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gac gac tcc gga aat 99
Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn
15 20 25

gga ttg gag aat ctt ttt tgc aag gca cat cac gag atg aag aac ccc 147
Gly Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro
30 35 40

aaa gac tct aaa ttg aac aag agg tgc ctt gac ggt ggt gaa att tgt 195

Lys Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys
 45 50 55
 ggt att ttg ttt cca agc tgc tgc agt ggg tgg tgc att gtt ctc gtc 243
 Gly Ile Leu Phe Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val
 60 65 70 75
 tgc gca tgaaactacc gtgatgtctt ctactcccct ctgtgctacc tggcttgatc 299
 Cys Ala
 tttgattggc gcgtgccctt cactgggttat gaacccccct gatccgactc tctggcggcc 359
 tcggggggttc aacatccaaa taaagcgaca cgacaatgac aaaaaaaaaa aaaaaaaaaa 419
 aaaaaaaaaa 427

<210> 119
 <211> 77
 <212> PRT
 <213> Conus marmoreus

<400> 119

Met Lys Leu Thr Ser Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro
 50 55 60

Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
 65 70 75

<210> 120
 <211> 26
 <212> PRT
 <213> Conus marmoreus
 <220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
 mo-Trp

<400> 120

Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
 1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala

00321 4696760

20

25

<210> 121
 <211> 470
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (70)..(303)

<400> 121
 gctagcacag tgaatttggc ttcacagttt tccactgtcg tctttggcat catccaaaac 60
 atcaccaag atg aaa ctg acg tgc atg atg atc gaa gca gag ctg ttc ttg 111
 Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu
 1 5 10
 acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag 159
 Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
 15 20 25 30
 aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc gaa gcc tct 207
 Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45
 aaa ttg aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt 255
 Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
 50 55 60
 gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cct ata 303
 Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
 65 70 75
 taactaccgt gatgtcttct actccctctt gtgctgcctg gcttgatctt tgattggcgc 363
 gtgcccttca ctggttatga accccctga tccgactctc ttgcggcctc aggggttcaa 423
 catccaaata aagcgacacg aaaatgaaaa aaaaaaaaaa aaaaaaa 470

<210> 122
 <211> 78
 <212> PRT
 <213> Conus marmoreus

<400> 122

Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 20 25 30
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
 50 55 60

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Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
65 70 75

<210> 123
<211> 27
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 2 and 26 may be Pro or hydroxy-Pro; Xaa at residues 6 and 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 123

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Xaa Ile
20 25

<210> 124
<211> 470
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (67)..(312)

<400> 124
ttgcacggtg aatttcgctt atatttttct actgtogtct ttggcatcat ccaaaacatc 60
accaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 108
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
1 5 10
acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta ttg 156
Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu
15 20 25 30
gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc 204
Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala
35 40 45
tct aaa ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt 252
Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe
50 55 60
tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc 300
Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe
65 70 75
ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattccct ctgtgctacc 352
Leu Trp Cys Ala
80
tggccttgatc ttgattggc gcgtgccctt cagtggttat gaacccccct gatccgactc 412

0032221 2694650

<400> 127
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gca ttg gag aat 96
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn
 20 25 30

ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc tct aaa 144
 Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
 35 40 45

ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt tgt ggc 192
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
 50 55 60

ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc ctc tgg 240
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
 65 70 75 80

tgc gca taaaactgcc gtgatgtctt ctctccct c 277
 Cys Ala

<210> 128
 <211> 82
 <212> PRT
 <213> Conus striatus

<400> 128

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn
 20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
 35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
 50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
 65 70 75 80

Cys Ala

<210> 129
 <211> 30
 <212> PRT
 <213> Conus striatus

<220>
 <221> SITE

009937 13300

<222> (1)..(30)

<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp

<400> 129

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 130

<211> 277

<212> DNA

<213> Conus omaria

<220>

<221> CDS

<222> (1)..(246)

<400> 130

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gaa aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

ott tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

ttg aac acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc 192
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

atg ata aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

tgc gcc taaaactgcc gtgatgtctt ctctccct c 277
Cys Ala

<210> 131

<211> 82

<212> PRT

<213> Conus omaria

<400> 131

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

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Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

tgc gcc taaaactgcc gtgatgtctt ctctccct c
Cys Ala

277

<210> 134
<211> 82
<212> PRT
<213> Conus aulicus

<400> 134

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

Cys Ala

<210> 135
<211> 30
<212> PRT
<213> Conus aulicus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 135

Asp Xaa Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

<210> 136
<211> 685
<212> DNA

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<213> Conus marmoreus

<220>

<221> CDS

<222> (111)..(212)

<400> 136

ggtcgacatc atcatcatca tcgatccatc tgtccatcca tctattcatt cattcgtggc 60

caaaactgtaa taaataatgc aagtctctct ttctgtttgt atctgacaga ttg aac 116
Leu Asn
1

acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc atg ata 164
Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile
5 10 15

aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc tgc gcc 212
Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala
20 25 30

taaaactgcc gtgatgtctt ctcttcccct ctagtagtag taggcggccg ctctagagga 272

tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc acctaaattc 332

aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt taccctaactt 392

aatgccttg cagcacatcc ccctttcgcc agctggcgta atagcgaaga ggcccgacc 452

gatgcctt cccaacagtt gcgcagcctg aatggcgaat gggacgcgcc ctgtagcggc 512

gcattaagcg cggcgggtgt ggtggttac cgcagcgt gaccgctac acttgccagc 572

gocctagcgc ccgtcctttt cgctttcttc ctccctttct cgccacgttc gccggctttt 632

cccgtaagc tctaaatcgg gggctccttt aggtccgat ttaagtgtt tac 685

<210> 137

<211> 34

<212> PRT

<213> Conus marmoreus

<400> 137

Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
1 5 10 15

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
20 25 30

Cys Ala

<210> 138

<211> 30

<212> PRT

<213> Conus marmoreus

<220>

<221> SITE

003221" 4694260

<222> (1)..(30)
 <223> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 138

Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
 20 25 30

<210> 139
 <211> 126
 <212> DNA
 <213> Conus regius

<220>
 <221> CDS
 <222> (1)..(96)

<400> 139
 ttg aac cag aga gac tgc ctt agt aaa aac gct ttc tgt gcc tgg ccg 48
 Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
 1 5 10 15

ata ctt gga cca ctg tgc tgc agt ggc tgg tgc tta tac gtc tgc atg 96
 Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
 20 25 30

taaaactgcc gtgatgtctt ctatcccctc 126

<210> 140
 <211> 32
 <212> PRT
 <213> Conus regius

<400> 140

Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
 1 5 10 15

Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
 20 25 30

<210> 141
 <211> 28
 <212> PRT
 <213> Conus regius

<220>
 <221> SITE
 <222> (1)..(28)
 <223> Xaa at residues 11 and 22 may be Trp or bromo-Trp; Xaa at residues 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 150

Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr
 20 25

<210> 151
 <211> 412
 <212> DNA
 <213> Conus purpurascens

<220>
 <221> CDS
 <222> (1)..(243)

<400> 151
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30
 ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45
 gac aaa aag gaa gcc tgc tat gcg cct ggt act ttt tgt ggc ata aag 192
 Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 ccc ggg cta tgc tgc agt gag ttt tgt ctc ccg ggc gtc tgc ttc ggt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
 65 70 75 80
 ggt taactgcgct gatgtcttct actccctct gtgctacctg gcttgatctt 293
 Gly
 tgatcggcgt gtgccttcca ctggttatga acccactgat cttacctctc ttgaaggacc 353
 tctgggggtcc agcatccaaa taagcgacat cccaatgaaa aaaaaaaaaa aaaaaaaaaa 412

<210> 152
 <211> 81
 <212> PRT
 <213> Conus purpurascens

<400> 152

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

003221 496460

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45

Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
 65 70 75 80

Gly

<210> 153
 <211> 29
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
 o or hydroxy-Pro

<400> 153

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
 20 25

<210> 154
 <211> 29
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
 o or hydroxy-Pro

<400> 154

Xaa Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
 20 25

008227" 2E964260

<210> 155
 <211> 29
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 155

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ala Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
 20 25

<210> 156
 <211> 29
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 156

Xaa Ala Cys Xaa Ala Xaa Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
 20 25

<210> 157
 <211> 289
 <212> DNA
 <213> Conus magus

<220>
 <221> CDS
 <222> (1)..(252)

<400> 157

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tot aaa ttg 144

003327 7E96460

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt 192
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
 50 55 60

cca gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80

gtt gat tct ggc taacagtgtg cgttgggttag tgcctctcc tcccctc 289
 Val Asp Ser Gly

<210> 158
 <211> 84
 <212> PRT
 <213> Conus magus

<400> 158

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80

Val Asp Ser Gly

<210> 159
 <211> 32
 <212> PRT
 <213> Conus magus

<220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
 hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
 Xaa at residue 25 may be Trp or bromo-Trp

<400> 159

Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu

0082221 12200

1 5 10 15
 Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser
 20 25 30

<210> 160
 <211> 273
 <212> DNA
 <213> Conus magus

<220>
 <221> CDS
 <222> (1)..(249)

<400> 160
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
 Phe Pro Lys Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa 192
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 cca gga ctt tgc tgc agc gcg ata tgc tta tgc ttt gtc tgc ata tca 240
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80
 ttt gat ttt tgattgatgt cttctcctcc cctc 273
 Phe Asp Phe

<210> 161
 <211> 83
 <212> PRT
 <213> Conus magus

<400> 161
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser

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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30
 ttt ccg aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac cag aga gaa gcc tgc tat aat gct ggt aca ttt tgt ggc atc aaa 192
 Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 cca gga ctt tgc tgc agc gcg ata tgc tta tcg ttt gtc tgc ata tca 240
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80
 ttt gat ttg attgatgtct tctcctcccc tc 271
 Phe Asp Leu

<210> 167
 <211> 83
 <212> PRT
 <213> Conus magus

<400> 167

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
 20 25 30
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
 50 55 60
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
 65 70 75 80

Phe Asp Leu

<210> 168
 <211> 32
 <212> PRT
 <213> Conus magus
 <220>
 <221> SITE
 <222> (1)..(32)
 <223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residue

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4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro

<400> 168

Xaa Ala Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
20 25 30

<210> 169

<211> 272

<212> DNA

<213> Conus ermineus

<220>

<221> CDS

<222> (1)..(243)

<400> 169

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

ggt taactgcgct gatgtcttct cctccctc 272
Gly

<210> 170

<211> 81

<212> PRT

<213> Conus ermineus

<400> 170

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

003227 296460

<220>
 <221> CDS
 <222> (1)..(246)

<400> 175
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc act 48
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga gaa ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
 Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
 50 55 60
 cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 att gat tgatgtcttc tcctcccctc 266
 Ile Asp

<210> 176
 <211> 82
 <212> PRT
 <213> Conus striatus

<400> 176
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
 1 5 10 15
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
 65 70 75 80
 Ile Asp

<210> 177
 <211> 31

003231.496460

<212> PRT
<213> Conus striatus

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 177

Xaa Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
20 25 30

<210> 178
<211> 266
<212> DNA
<213> Conus striatus

<220>
<221> CDS
<222> (1)..(246)

<400> 178

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc act 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

att gat tgatgtcttc tcttccccctc 266
Ile Asp

<210> 179
<211> 82
<212> PRT
<213> Conus striatus

<400> 179

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

003227.169460

<212> DNA
<213> Conus catus

<220>
<221> CDS
<222> (1)..(234)

<400> 182
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

cca gga ctc tgc tgc agc gag ctt tgc ctg gtt tgg tgc aca 234
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
65 70 75

tgagtgtctat tcttctggta cattttgtgg cttcaacgga ggactctgct gcagcaacct 294
ttgcttattt tcgtgtgctt aacatttctgt gatgtcttct ctattccct c 345

<210> 183
<211> 78
<212> PRT
<213> Conus catus

<400> 183
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
65 70 75

<210> 184
<211> 27
<212> PRT
<213> Conus catus

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 184

Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
 1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr
 20 25

<210> 185
 <211> 345
 <212> DNA
 <213> Conus catus

<220>
 <221> CDS
 <222> (1)..(234)

<400> 185
 atg aaa ctg acg tgt atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 tgg aca ttc gtc acg gct gat gaa tcc aga tat gga ctg aag aat ctt 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
 20 25 30
 ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45
 aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
 50 55 60
 oca gga ctc tgc tgc agc gag ctt tgc ctg ggt tgg tgc aca 234
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
 65 70 75
 tgagtgttat tctactggta cttttgtgg cttcaacgga ggactctgct gcagcaacct 294
 ttgcttattt tcgtgtgctt aacatttcgt gatgtcttct ctattcccct c 345

<210> 186
 <211> 78
 <212> PRT
 <213> Conus catus

<400> 186

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

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Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
65 70 75

<210> 187

<211> 27

<212> PRT

<213> Conus catus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 187

Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Gly Xaa Cys Thr
20 25

<210> 188

<211> 266

<212> DNA

<213> Conus distans

<220>

<221> CDS

<222> (1)..(246)

<400> 188

atg aaa ctg acg tgt ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctc 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

tct ccg aag gca cct cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

aac aag aga tat gag tgc tat ctc ctc gta cat ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
50 55 60

0082227 2964637 122800

<213> Conus regius

<220>

<221> CDS

<222> (1)..(93)

<400> 191

ttg	agc	aag	aga	gac	tgc	ctt	cct	gac	tac	acg	att	tgt	gcc	ttc	aat	48
Leu	Ser	Lys	Arg	Asp	Cys	Leu	Pro	Asp	Tyr	Thr	Ile	Cys	Ala	Phe	Asn	
1				5					10					15		

atg	ggt	ctg	tgc	tgc	agc	gac	aag	tgc	atg	ctc	gtc	tgc	ctg	cgc		93
Met	Gly	Leu	Cys	Cys	Ser	Asp	Lys	Cys	Met	Leu	Val	Cys	Leu	Pro		
			20					25					30			

tgatgtcttc	tcctcccctc	113
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<210> 192

<211> 31

<212> PRT

<213> Conus regius

<400> 192

Leu	Ser	Lys	Arg	Asp	Cys	Leu	Pro	Asp	Tyr	Thr	Ile	Cys	Ala	Phe	Asn
1				5					10					15	

Met	Gly	Leu	Cys	Cys	Ser	Asp	Lys	Cys	Met	Leu	Val	Cys	Leu	Pro
			20					25					30	

<210> 193

<211> 27

<212> PRT

<213> Conus regius

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residues 5 and 27 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 193

Asp	Cys	Leu	Xaa	Asp	Xaa	Thr	Ile	Cys	Ala	Phe	Asn	Met	Gly	Leu	Cys
1				5					10					15	

Cys	Ser	Asp	Lys	Cys	Met	Leu	Val	Cys	Leu	Xaa
			20					25		

<210> 194

<211> 116

<212> DNA

<213> Conus regius

<220>

<221> CDS

<222> (1)..(96)

<400> 194

003301 469460

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45

ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
 50 55 60

caa tgc tgc agt ggc tgg tgc att ttc gcc tgc ctc taaaactgtc 238
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
 65 70 75

gtgatgtctt ctctctccct c 259

<210> 198
 <211> 76
 <212> PRT
 <213> Conus gloriamaris

<400> 198

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
 20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
 50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
 65 70 75

<210> 199
 <211> 24
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> SITE
 <222> (1)..(24)
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
 bromo-Trp

<400> 199

Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
 1 5 10 15

Gly Xaa Cys Ile Phe Ala Cys Leu
 20

003221" 469460

Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn
35 40 45

Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
50 55 60

Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
65 70 75

<210> 205
<211> 24
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(24)
<223> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 5 may be Trp or bromo-Trp; Xaa at residue 11 may be Pro o
r hydroxy-Pro

<400> 205

Cys Phe Xaa Ser Xaa Val Ala Cys Xaa Ser Xaa Lys Arg Cys Cys Ser
1 5 10 15

His Val Cys Leu Phe Val Cys Thr
20

<210> 206
<211> 253
<212> DNA
<213> Conus distans

<220>
<221> CDS
<222> (1)..(228)

<400> 206

atg aaa ctg acg tgt atg ttg atc atc gct gtg ctg ttc ctg acg gcc 48
Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgt caa ctc tct aca aat gcg agt tac gcc aga agt aag cag aag cat 96
Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
20 25 30

cgt gtt ctg agg tcg act gac aaa aac tcc aag ttg acc cag cgt tgc 144
Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
35 40 45

aat gaa gct caa gaa cat tgc act caa aat cct gac tgc tgc agt gag 192
Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu
50 55 60

tct tgc aat aag ttt gtc ggc aga tgc ttg tca gac tgatctgatg 238
Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
65 70 75

002227 4696460

Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
65 70 75 80

Cys Ala

<210> 223
<211> 31
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residues 8 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 26 may be Pro or hydroxy-Pro

<400> 223

Asp Cys Gln Xaa Lys Xaa Asp Xaa Cys Xaa Val Xaa Phe Leu Gly Ser
1 5 10 15

Arg Xaa Cys Cys Asp Gly Phe Ile Cys Xaa Ser Phe Phe Cys Ala
20 25 30

<210> 224
<211> 271
<212> DNA
<213> Conus dalli

<220>
<221> CDS
<222> (1)..(252)

<400> 224

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ttg ttc ctg aca gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat cat 96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

ttt tgg aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg 144
Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

gag aaa agg gat tgc caa ggc gaa tgg gag ttt tgt ata gta ccg gtc 192
Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

ctt gga ttt gtg tat tgc tgc ccc tgg ctt atc tgt ggc cct ttc gtc 240
Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

tgc gtt gat atc tgatgtcttc tatccccctc 271
Cys Val Asp Ile

0002221 25957450

1	5	10	15
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Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val
 20 25 30

<210> 242
 <211> 552
 <212> DNA
 <213> Conus omaria

<220>
 <221> CDS
 <222> (149)..(271)

<400> 242
 aaagccggtgta cgcctgcagg tacccggtccg gaattcccgg gtcgacatca tcatcatcat 60
 cgatccatct gtccatccat ccattcattc attcactgcc aaactgtcat aaatatttga 120
 gtctctcttt ctgtttttat ctgacaga ttg aac gag aga gac tgc ott aat 172
 Leu Asn Glu Arg Asp Cys Leu Asn
 1 5
 gtt gat tat ttt tgt ggc ata ccg ttt gtg aac aac ggg cta tgc tgc 220
 Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys
 10 15 20
 agt ggc aat tgt gtt ttt tgt ctg cac acc cca agg gaa gta aaa ctg 268
 Ser Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu
 25 30 35 40
 ccg tgatgtcttc ttttccctc tagtagtagt aggcggccgc tctagaggat 321
 Pro
 ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca cctaaattca 381
 attcactggc cgctgtttta caacgtcgtg actgggaaaa ccctggcggtt acccaactta 441
 atcgcccttg agcacatccc cctttcgcca gctggcgtaa tagcgaagag gcccgcccg 501
 atcgcccttc ccaacagttg cgcagcctga atggcgcaatg ggacgcgccc t 552

<210> 243
 <211> 41
 <212> PRT
 <213> Conus omaria

<400> 243

Leu Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro
 1 5 10 15

Phe Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu
 20 25 30

His Thr Pro Arg Glu Val Lys Leu Pro
 35 40

<210> 244
 <211> 37
 <212> PRT

0082221" 4096460

<220>
 <221> SITE
 <222> (1)..(29)
 <223> Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 253

Xaa Cys Thr Ala Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser
 1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys Ile
 20 25

<210> 254
 <211> 133
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (2)..(100)

<400> 254

a ttg gac aag aaa gag tgc act acc aat ggt gaa ttt tgt ggc ata tcg 49
 Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
 1 5 10 15

gtc ttt gca agc ttc cta tgc tgc agt ggc ctg tgt gta ttc gtc tgc 97
 Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
 20 25 30

atc tagctgaact gccgtgatgt cttctcttcc cct 133
 Ile

<210> 255
 <211> 33
 <212> PRT
 <213> Conus radiatus

<400> 255

Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
 1 5 10 15

Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
 20 25 30

Ile

<210> 256
 <211> 29
 <212> PRT
 <213> Conus radiatus

003227 256460

Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys
35 40 45

Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
50 55 60

Ser Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
65 70 75 80

Pro Tyr Arg Cys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala
85 90 95

<210> 265
<211> 28
<212> PRT
<213> Conus delessertii

<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residues 4 and 14 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 15 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 265

Asp Cys Ile Xaa Gly Gly Xaa Asn Cys Asp Val Phe Arg Xaa Xaa Arg
1 5 10 15

Cys Cys Ser Gly Xaa Cys Ile Leu Leu Cys Ala
20 25

<210> 266
<211> 1009
<212> DNA
<213> Conus striatus

<220>
<221> CDS
<222> (147)..(233)

<220>
<221> misc_feature
<222> (1)..(1009)
<223> n may be any nucleotide

<400> 266
gctggttcgc ctgcaggtac cgggtccggaa ttcccgggtc gacatcatca tcatcgatcc 60
atctgtccat ccatctattc attcattcat tcgtgccaa actgtattaa atattcaagt 120
ctctctttct gtttgtgtct aacaga ttg aga tgg tgc att cct agt ggt gaa 173
Leu Arg Trp Cys Ile Pro Ser Gly Glu
1 5

ctt tgt ttc cgc tcg gat cac ata gga tgc tgc agt ggc aag tgc gca 221
Leu Cys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala

<400> 281
ggatcttgca cggatgaattt cgcttcatat tttctactg tcgtcttttg catcatocaa 60

aacatcacca ag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 111
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
 1 5 10

ttg acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta 159
 Leu Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val
 15 20 25

ttg gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa 207
 Leu Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu
 30 35 40 45

gcc tct aaa ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat 255
 Ala Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp
 50 55 60

ttt tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc 303
 Phe Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys
 65 70 75

ttc ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattccct ctgtgctacc 358
 Phe Leu Trp Cys Ala
 80

tggttgatc tttgattggc gcgtgccctt cagtgggtat gaacccccct gagccgactc 418

tctgggggcc tcgggggttc aacatccaaa taaagcgaca acacaatcac aagtaaaaaa 478

<210> 282

<211> 82

<212> PRT

<213> Conus geographus

<400> 282

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
 20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
 35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
 50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
 65 70 75 80

Cys Ala

<210> 283

<211> 30

<212> PRT

00822T" 4696460

<213> Conus geographus

<220>

<221> SITE

<222> (1)..(30)

<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp

<400> 283

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 284

<211> 318

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (3)..(164)

<220>

<221> misc_feature

<222> (1)..(318)

<223> n may be any nucleotide

<400> 284

gc tgc agg tcg act cta gag gcg ttg gag aat ctt tat ctg aag gca 47
Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala
1 5 10 15

cat cat gaa atg aac aac ccc gaa gac tct gaa ttg aac aag agg tgc 95
His His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys
20 25 30

tat gat agt ggg aca agt tgt aac act gga aac caa tgc tgc agt ggc 143
Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly
35 40 45

tgg tgc att ttc gtc tgc ctc taaaactgcc gtgatgtctt ctactccct 194
Trp Cys Ile Phe Val Cys Leu
50

ctgtgctacc tacctggctt gatctttgat tggcgcgtgc ccttcactgg ttatgaaccc 254

ctctgatccg actctctggg ggctctgggg atccaacatc aaaatanagc gacagcacia 314

tcac 318

<210> 285

<211> 54

<212> PRT

<213> Conus textile

<220>

<221> misc_feature

00222T" 42964/50

<222> (1)..(318)

<223> n may be any nucleotide

<400> 285

Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala His
1 5 10 15

His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys Tyr
20 25 30

Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp
35 40 45

Cys Ile Phe Val Cys Leu
50

<210> 286

<211> 24

<212> PRT

<213> Conus textile

<220>

<221> SITE

<222> (1)..(24)

<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or bromo-Trp

<400> 286

Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
1 5 10 15

Gly Xaa Cys Ile Phe Val Cys Leu
20

<210> 287

<211> 480

<212> DNA

<213> Conus quercinus

<220>

<221> CDS

<222> (52)..(333)

<400> 287

gcttcgtatt tctccgctgt cttccttggc atcacccaaa acatcaccaa g atg aaa 57
Met Lys
1

ctg.acg tgc atg atg atc gtt gct ctg ctg ttc ttg acc gcc tgg aca 105
Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala Trp Thr
5 10 15

ttc gtc acg gct gtt gac tcc aaa aat gaa ctg gag aac aga gga gga 153
Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg Gly Gly
20 25 30

aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta taaaactacc 241

<222> (7)..(240)

<400> 296

ggatcc atg aaa ctg acg tgt atg gtg atc gtt gct gtg cta ttc ttg 48
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gcc tcg gct gat gac tcc aga aat gga ttc gag aat cga aat gga 96
 Thr Ala Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly
 15 20 25 30

gaa cga aac gaa aac gaa atg aag aac ctc gaa gcc tct aaa ttg aac 144
 Glu Arg Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn
 35 40 45

agg aga gac ggc gat tgc gtt gat ggt ggt gaa ttt tgt ggc ttt ccg 192
 Arg Arg Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro
 50 55 60

aaa att gga ggg cca tgc tgt agt ggc tgg tgc ttt ttc gtc tgc tta 240
 Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

taaaactgcc atgatgtctt ctacccccct ctgtgctacc tgacttgatc tttgattggc 300

gtgtgccctt cactgggttat gaacccctct gatccgactc tctggaggcc tcgggggtcc 360

aacatccaaa taaagcgaca gcaaaaaaaaa aaaaaaaaaa aa 402

<210> 297

<211> 78

<212> PRT

<213> Conus quercinus

<400> 297

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly Glu Arg
 20 25 30

Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn Arg Arg
 35 40 45

Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro Lys Ile
 50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
 65 70 75

<210> 298

<211> 30

<212> PRT

<213> Conus quercinus

<220>

<221> SITE

00822T 4E9H460

<400> 300

acc gcc tgg aca ttc gtc acg gct gac tcc ata cgt gca ctg gag gat 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp

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<210> 303
<211> 80
<212> PRT
<213> Conus arenatus
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<400> 303

Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp Phe Phe
20 25 30

Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro Tyr Lys
50 55 60

<210>	304
<211>	30
<212>	PRT
<213>	Conus arenatus

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<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro; Xaa at residues 8 and 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or brom

```

o-Trp

<400> 304

Asp Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn
 1 5 10 15

Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
 20 25 30

<210> 305

<211> 281

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (7)..(234)

<400> 305

ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gtt gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu
 1 5 10

acc gcc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag 96
 Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu
 15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45

aaa ttg aac gag agg tgc ctt gaa aag ggt gta ctt tgt gat ccg agt 192
 Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser
 50 55 60

gct gga aac tgc tgt agt ggc gaa tgc gtt tta gtc tgc ctc 234
 Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
 65 70 75

taaaactacc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

<210> 306

<211> 76

<212> PRT

<213> Conus arenatus

<400> 306

Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser Ala Gly

09749637-122800

60

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<210> 309
<211> 78
<212> PRT
<213> Conus arenatus
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gat aga ggc ata tgg ggg gaa cct ttg tcg aag gca cgt gac gaa atg 144
Asp Arg Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met

```

<210> 312
<211> 79
<212> PRT
<213> Conus tessulatus

<400> 312

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu Thr Ala
1          5          10          15

Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asp Arg
          20          25          30

Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met Asn Pro
          35          40          45

Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys Gly Leu
          50          55          60

Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys Phe
65          70          75

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<210> 313
<211> 26
<212> PRT
<213> Conus tessulatus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 7 may be Trp or bromo-Trp; Xaa at residues
      4 and 17 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Tyr,
      125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
      Tyr

<400> 313

Asp Cys Xaa Xaa Gln Xaa Xaa Phe Cys Gly Leu Gln Arg Gly Cys Cys
1          5          10          15

```


Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr Lys Leu
35 40 45

ctg ttt gaa gca caa tgc tgc gat ggc tgg tgc ttt ttc gtc tgc atg 240
Leu Phe Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
65 70 75

taaaactgcc gtgatgtctt ctactctcct ctgtgctacc tgcctgatac ttgattggc 300
 tcgcgccctt cattgggttat gaacccctct gatcctactc tctggaggcc tcaggggtcc 360
 agcatctaaa taaagcgaca tcacaatcaa aaaaaaaaaa aaaaaaaaaa 408

<210> 318
 <211> 78
 <212> PRT
 <213> Conus imperialis

<400> 318

Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu Thr Ala
 1 5 10 15

Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu Asn Leu
 20 25 30

Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met Leu Phe
 50 55 60

Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
 65 70 75

<210> 319
 <211> 27
 <212> PRT
 <213> Conus imperialis

<220>
 <221> SITE
 <222> (1)..(27)
 <223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 5, 7 and
 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 21 may be Trp
 or bromo-Trp

<400> 319

Xaa Cys Arg Val Xaa Gly Xaa Ile Cys Gly Met Leu Phe Xaa Ala Gln
 1 5 10 15

Cys Cys Asp Gly Xaa Cys Phe Phe Val Cys Met
 20 25

<210> 320
 <211> 281
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (7)..(234)

003327 " 446460

<400> 320
 ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag 96
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu
 15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
 35 40 45

aaa ttg aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt ccg gga 192
 Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly
 50 55 60

ttt gga gat tgc tgc act ggc ttc tgc ctt tta gtc tgc atc 234
 Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
 65 70 75

taaaactgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

<210> 321
 <211> 76
 <212> PRT
 <213> Conus characteristicus

<400> 321
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 35 40 45

Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly Phe Gly
 50 55 60

Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
 65 70 75

<210> 322
 <211> 25
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> SITE
 <222> (1)..(25)
 <223> Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residu
 e 6 may be Glu or gamma-carboxy-Glu

<400> 322

Cys Val Asp Xaa Gly Xaa Phe Cys Gly Xaa Gly Phe Gly Asp Cys Cys
1 5 10 15

Thr Gly Phe Cys Leu Leu Val Cys Ile
20 25

<210> 323
<211> 287
<212> DNA
<213> Conus miliaris

<220>
<221> CDS
<222> (7)..(240)

<400> 323
ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ttg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc atg gct gat gac tcc aga aat gat ttg gag 96
Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu
15 20 25 30

aat ctt ttt ctg aag gca cgt cat gaa atg aag aac ccc gaa gct tct 144
Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac aag aga tgc ctt cca aat ggt gta ctt tgt gat ctg gga 192
Lys Leu Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly
50 55 60

tct cca cca tac tgc tgc agt ggc tgg tgc gcg atc gtc gtc tgc atc 240
Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile
65 70 75

taaaactgtc gtcattgtctt ctactcccat ctgtgctacc cctcgag 287

<210> 324
<211> 78
<212> PRT
<213> Conus miliaris

<400> 324

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu
20 25 30

Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly Ser Pro
50 55 60

Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile

003331" 4664260

75

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<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 3, 13 and 14 may be Pro or hydroxy-Pro; Xaa at re
sidue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sul
pho-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-T
rp
```

Cys Ser Gly Xaa Cys Ala Ile Val Val Cys Ile
20 25

<220>
<221> CDS
<222> (7)..(240)

taaaactgcc gtgatgtgtt ctactcccat ctgtgctacc cctcgag 287

<400> 327

aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta 237
Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

```
<210> 330
<211> 77
<212> PRT
<213> Conus lividus
```

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

```
<210> 331
<211> 26
<212> PRT
<213> Conus lividus
```

```
<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and
      12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 ma
      y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
      O-phospho-Tyr
```

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
20 25

$\langle 210 \rangle$	332
$\langle 211 \rangle$	281
$\langle 212 \rangle$	DNA

<221> SITE

<222> (1)..(25)

<223> Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and 22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 334

Cys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Xaa Cys Cys
1 5 10 15

Ser Gly Phe Cys Leu Xaa Val Cys Ile
20 25

<210> 335

<211> 293

<212> DNA

<213> *Conus generalis*

<220>

<221> CDS

<222> (7)..(249)

<400> 335

ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg cta ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac acc aga tat aaa ctg gag 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu
15 20 25 30

aat cct ttt ctg aag gca cgc aac gaa ctg cag aaa cac gaa gcc tct 144
Asn Pro Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser
35 40 45

caa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg acg 192
Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr
50 55 60

cgc ttt ctt gga gca tac tgc tgc ggt ggc att tgc ctt att gtc tgc 240
Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys
65 70 75

ata gaa acg taaaggcttg atgtcttcta ctcccatctg tgctaccct cgag 293
Ile Glu Thr
80

<210> 336

<211> 81

<212> PRT

<213> *Conus generalis*

<400> 336

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu Asn Pro
20 25 30

003222T" / E964/60

Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser Gln Leu
35 40 45

Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr Pro Phe
50 55 60

Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Glu
65 70 75 80

Thr

<210> 337
<211> 30
<212> PRT
<213> Conus generalis

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 337

Gly Cys Leu Asp Xaa Gly Xaa Phe Cys Gly Thr Xaa Phe Leu Gly Ala
1 5 10 15

Xaa Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Xaa Thr
20 25 30

<210> 338
<211> 400
<212> DNA
<213> Conus episcopatus

<220>
<221> CDS
<222> (7)..(234)

<400> 338
ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 96
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
15 20 25 30

aat ctt ttt tcg aat gta cat cac gaa atg aag aac ctc gaa gac tct 144
Asn Leu Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser
35 40 45

aaa ttg gac aag aag tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt 192
Lys Leu Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu
50 55 60

<220>

<221> CDS

<222> (7)..(240)

<400> 341

ggatcc atg aaa ctg acg tgc gtg gtg atc att gct gtg ctg ttc ttg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
 1 5 10

acc gcc tgg aca ttc gtc atg gct gat gac ccc aga gat gaa ccg gag 96
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu
 15 20 25 30

gca cgt gac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc 144
 Ala Arg Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly
 35 40 45

tgc ctt gca gtt gat tat ttt tgc ggc ata ccg ttt gtg agc aac ggc 192
 Cys Leu Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly
 50 55 60

cta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca ccc caa ggg aag 240
 Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
 65 70 75

taaaactgcc gtgacgtctt ctactccct ctgtgctacc tggcttgatc tttgattggc 300

gtgtgcactt cactgggttat gaacccctct gatcctactc totgaagacc tctgggggtcc 360

aacatccaaa taaagcgaca tccccaaaaa aaaaaaaaaa aaaa 404

<210> 342

<211> 78

<212> PRT

<213> Conus episcopatus

<400> 342

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
 20 25 30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
 35 40 45

Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly Leu Cys
 50 55 60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
 65 70 75

<210> 343

<211> 31

<212> PRT

<213> Conus episcopatus

0092227 2E964260

<220>
 <221> SITE
 <222> (1)..(31)
 <223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydroxy-Pro

<400> 343

Gly Cys Leu Ala Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Ser Asn
 1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
 20 25 30

<210> 344
 <211> 202
 <212> DNA
 <213> Conus achatinus

<220>
 <221> CDS
 <222> (85)..(171)

<400> 344
 cgatcctctg tcctccatct attattattc gctgccaaac tgtgttaaatt attcaagtct 60

ctctttctgt ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat 111
 Leu Arg Trp Cys Ile Pro Arg Gly Asp
 1 5

ctt tgt ttc ccc tgc gat cgc ata caa tgc tgc agt ggc aag tgc aca 159
 Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr
 10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctctccct c 202
 Phe Val Cys Met

<210> 345
 <211> 29
 <212> PRT
 <213> Conus achatinus

<400> 345

Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg
 1 5 10 15

Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
 20 25

<210> 346
 <211> 27
 <212> PRT
 <213> Conus achatinus

<220>
 <221> SITE
 <222> (1)..(27)

008221" 4E964260

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

<400> 346

Xaa Cys Ile Xaa Arg Gly Asp Leu Cys Phe Xaa Ser Asp Arg Ile Gln
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 347

<211> 202

<212> DNA

<213> Conus achatinus

<220>

<221> CDS

<222> (85)..(171)

<400> 347

cgatcctctg tctcctcctc tcattcattc gctgccaaac tgtattaaat attcgaatct 60

ctctttctgt ttgtgtctga caga ttg aga ggg tgc gtt cct agt ggt gaa 111
Leu Arg Gly Cys Val Pro Ser Gly Glu
1 5

att tgt tac ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca 159
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr
10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctctcccat c 202
Phe Val Cys Met

<210> 348

<211> 29

<212> PRT

<213> Conus achatinus

<400> 348

Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 349

<211> 27

<212> PRT

<213> Conus achatinus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

00822T 496460

Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg
50 55 60


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<210> 352
<211> 27
<212> PRT
<213> Conus bullatus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 2 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residues 6 and 14 may be Pro or hydroxy-Pro
```

Asp Xaa Cys Ser Ala Xaa Gly Ala Phe Cys Leu Ile Arg Xaa Gly Leu
1 5 10 15

```
<210> 353
<211> 276
<212> DNA
<213> Conus bullatus
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<220>
<221> CDS
<222> (1)..(246)
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[illegible]

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<210> 354
<211> 82
<212> PRT
<213> Conus bullatus
```



```
<210> 357
<211> 79
<212> PRT
<213> Conus striolatus
```

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
50 55 60

Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
65 70 75

```
<210> 358
<211> 28
<212> PRT
<213> Conus striolatus
```

```
<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residue 11 may be Trp or bromo-Trp; Xaa at residues 12 and
16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.
```

Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
1 5 10 15

Leu Cys Cys Ser Arg Leu Cys Leu Xaa Val Cys Met
20 25

```

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1          5          10          15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
          20          25          30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
          35          40          45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
          50          55          60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65          70          75          80

Phe Ser

```

```
<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
Glu or gamma-carboxy-Glu
```

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

```
<210> 362
<211> 289
<212> DNA
<213> Conus consors
```

```
<220>
<221> CDS
<222> (1)..(252)
```

[illegible]

<210>	363
<211>	84
<212>	PRT
<213>	Conus consors

```

<400> 365
cgatccatct gtccatccat ctattcattc attcgcgtgcc aaactgtatt aaatattcaa      60

gtctctcttt ctgtttgtgt ct aac aga ttg a,t agg tgc att cct agt ggt      112
                        Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
                        1          5          10

```

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactcccct c 206

```

<400>   371
cgatccatct gtccatccat ctattcattc attcgtgtc aaactgtatt aaatattcaa      60

gtctctcttt ctgttttgtgt ct aac aga ttg agt agg tgc att cct agt ggt      112
                        Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
                        1                      5                      10

gat ctt tgt ttc ooc tgc gat cac ata caa tgc tgc agt gcc aag tgc      160
Asp Leu Cys Phe      15 Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
                        20                      25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctctccct c      206
Ala Phe Val Cys Leu
                        30

```


<210> 372
 <211> 31
 <212> PRT
 <213> Conus circumcisis

<400> 372

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25 30

<210> 373
 <211> 26
 <212> PRT
 <213> Conus circumcisis

<220>
 <221> SITE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 373

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15

Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
 20 25

<210> 374
 <211> 206
 <212> DNA
 <213> Conus circumcisis

<220>
 <221> CDS
 <222> (83)..(175)

<400> 374
 cgatccatct gtccatccat ctattcattc attcgtgcc aaactgtatt aaatattcaa 60
 gtctctcttt ctgttttgtt ct aac aga ttg agt agg tgc att cct agt ggt 112
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
 1 5 10
 gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc gag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys
 15 20 25
 gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctcccct c 206
 Ala Phe Val Cys Leu
 30

<210> 375
 <211> 31
 <212> PRT
 <213> Conus circumcisis

<400> 375

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu
 20 25 30

<210> 376

<211> 26

<212> PRT

<213> Conus circumciscus

<220>

<221> SITE

<222> (1)..(26)

<223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu

<400> 376

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
 1 5 10 15

Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu
 20 25

<210> 377

<211> 206

<212> DNA

<213> Conus circumciscus

<220>

<221> CDS

<222> (83)..(175)

<400> 377

cgatccatct gtccatccat ctattcattc attcgtgtgc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
 1 5 10

gat ctt tgt ttc ccc tcg gat cac ata cga tgc tgc agt gcc aag tgc 160
 Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtott ctottcccat c 206
 Ala Phe Val Cys Leu
 30

<210> 378

<211> 31

<212> PRT

<213> Conus circumciscus

<400> 378

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25 30

<210>	385
<211>	27
<212>	PRT

<220>

<222> (1) .. (27)

<400> 385

Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
20 25

<211> 200

<212> DNA

 $\langle 220 \rangle$

<221> CDS

<400> 386

ctttctgttt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt 112
Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu
1 5 10

tgt ttc ccc tgc gat cac ata caa tgc tgc agt ggc aag tgc aca ttc 160
Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe
15 20 25

gtc tgc atg taaaactgcc gtgatgtctt ctctctccct c 200
Val Cys Met
30

<210> 387

<211> 31

<212> PRT

<400> 387

Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25 30

<210> 388

<211> 27

<212> PRT

<213> Conus circumcisis

 $\langle 220 \rangle$

<221> SITE

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser

35

40

45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

<210> 391

<211> 31

<212> PRT

<213> Conus monachus

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 391

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<210> 392

<211> 277

<212> DNA

<213> Conus stercusmuscarum

<220>

<221> CDS

<222> (1)..(246)

<400> 392

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc aca gct gat gac tcc ata aat gga ccg gag aat aga 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
20 25 30

cga ata tgg gag aaa ctt ttg ttg aag gca cgt gac gaa atg aag aac 144
Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
35 40 45

ccc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt 192
Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
50 55 60

ttc cgc tcg gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc 240
Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val

003333 4696460

<400> 393

Cys Leu

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<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be
      Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy
      -Glu
```

<400> 394

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<210> 395
<211> 266
<212> DNA
<213> Conus stercusmuscarum
```


<400> 395

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
20 25 30

aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cgt 192
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
50 55 60

cga gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

att gat tgatgtcttc tattcccttc 266
Ile Asp

```
<210> 396
<211> 82
<212> PRT
<213> Conus stercusmuscarum
```

<400> 396

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
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Ile Asp

<210>	397
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Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser
 35 40 45

Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro
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Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala
 65 70 75

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<220>
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 <222> (1)..(27)
 <223> Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bromo-Trp

<400> 400

Cys Arg Xaa Gly Gly Thr Val Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa
 1 5 10 15

Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala
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 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
 Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
 20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
 Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
 50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly

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80

272

<400> 402

Gly

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Met	Lys	Leu	Thr	Cys	Leu	Met	Ala	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala	
1				5				10					15			

cgg	aca	ttc	gtc	acg	gct	gat	gac	tcc	aga	aat	gga	ttg	gag	aat	ctt	96
Arg	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu	
			20					25					30			

tct	ccg	aag	gca	cgt	cac	gaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	tcg	144
Ser	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Ser	
		35					40					45				

aac	aag	aga	tat	gag	tgc	tat	tct	act	ggt	aca	ttt	tgt	ggc	atc	aac	192
Asn	Lys	Arg	Tyr	Glu	Cys	Tyr	Ser	Thr	Gly	Thr	Phe	Cys	Gly	Ile	Asn	
	50					55					60					

gga	gga	ctc	tgc	tgc	agc	aac	ctt	tgc	tta	ttt	ttc	gtg	tgc	tta	aca	240
Gly	Gly	Leu	Cys	Cys	Ser	Asn	Leu	Cys	Leu	Phe	Phe	Val	Cys	Leu	Thr	
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ttt	tcg	tgatgtcttc	tatccccctc													265
Phe	Ser															

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<211> 82

<212> PRT

<213> Conus striolatus

<400> 405

Met	Lys	Leu	Thr	Cys	Leu	Met	Ala	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala
1				5				10						15	

Arg	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu
			20					25					30		

Ser	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Ser
		35					40					45			

Asn	Lys	Arg	Tyr	Glu	Cys	Tyr	Ser	Thr	Gly	Thr	Phe	Cys	Gly	Ile	Asn
50						55					60				

Gly	Gly	Leu	Cys	Cys	Ser	Asn	Leu	Cys	Leu	Phe	Phe	Val	Cys	Leu	Thr
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Phe Ser

<210> 406

<211> 31

Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg

30

Xaa Lys Asn
35